OIPE

RAW SEQUENCE LISTING   DATE: 04/19/2002
PATENT APPLICATION: US/10/046,420   TIME: 16:05:07

Input Set : N:\Crf3\RULE60\10046420.raw
Output Set: N:\CRF3\04192002\J046420.raw

```
 1 <110> APPLICANT: Voellmy, Richard
 2 <120> TITLE OF INVENTION: MOLECULAR REGULATORY CIRCUITS TO ACHIEVE
 3       SUSTAINED ACTIVATION OF GENES OF INTEREST BY A SINGLE STRESS
 4 <130> FILE REFERENCE: 870109.409
 5 <140> CURRENT APPLICATION NUMBER: 10/046,420
 6 <141> CURRENT FILING DATE: 2002-04-19
 9 <150> PRIOR APPLICATION NUMBER: US/09/304,121
10 <151> PRIOR FILING DATE: 1999-05-03
13 <160> NUMBER OF SEQ ID NOS: 3
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2156
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapien
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (161)...(1747)
23 <400> SEQUENCE: 1
24       cgggcccgtt gcaagatggc ggcggccatg ctgggccccg gggctgtgtg tgcgcagcgg      60
25       gcggcggcgc ggcccggaag gctggcgcgg cgacggcgtt agcccggccc tcggcccctc     120
26       tttgcggccg ctccctccgc ctattccctc cttgctcgag atg gat ctg ccc gtg      175
27                                                    Met Asp Leu Pro Val
28                                                     1               5
29       ggc ccc ggc gcg gcg ggg ccc agc aac gtc ccg gcc ttc ctg acc aag      223
30       Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe Leu Thr Lys
31                    10              15                  20
32       ctg tgg acc ctc gtg agc gac ccg gac acc gac gcg ctc atc tgc tgg      271
33       Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu Ile Cys Trp
34                    25              30                  35
35       agc ccg agc ggg aac agc ttc cac gtg ttc gac cag ggc cag ttt gcc      319
36       Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly Gln Phe Ala
37                    40              45                  50
38       aag gag gtg ctg ccc aag tac ttc aag cac aac aac atg gcc agc ttc      367
39       Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met Ala Ser Phe
40                    55              60                  65
41       gtg cgg cag ctc aac atg tat ggc ttc cgg aaa gtg gtc cac atc gag      415
42       Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val His Ile Glu
43            70              75                  80                  85
44       cag ggc ggc ctg gtc aag cca gag aga gac gac acg gag ttc cag cac      463
45       Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp Thr Glu Phe Gln His
46                    90                  95                 100
47       cca tgc ttc ctg cgt ggc cag gag cag ctc ctt gag aac atc aag agg      511
48       Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu Glu Asn Ile Lys Arg
```

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```
49                    105              110              115
50    aaa gtg acc agt gtg tcc acc ctg aag agt gaa gac ata aag atc cgc    559
51    Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu Asp Ile Lys Ile Arg
52                    120              125              130
53    cag gac agc gtc acc aag ctg ctg acg gac gtg cag ctg atg aag ggg    607
54    Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val Gln Leu Met Lys Gly
55                    135              140              145
56    aag cag gag tgc atg gac tcc aag ctc ctg gcc atg aag cat gag aat    655
57    Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala Met Lys His Glu Asn
58        150              155              160              165
59    gag gct ctg tgg cgg gag gtg gcc agc ctt cgg cag aag cat gcc cag    703
60    Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg Gln Lys His Ala Gln
61                    170              175              180
62    caa cag aaa gtc gtc aac aag ctc att cag ttc ctg atc tca ctg gtg    751
63    Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe Leu Ile Ser Leu Val
64                    185              190              195
65    cag tca aac cgg atc ctg ggg gtg aag aga aag atc ccc ctg atg ctg    799
66    Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys Ile Pro Leu Met Leu
67                    200              205              210
68    aac gac agt ggc tca gca cat tcc atg ccc aag tat agc cgg cag ttc    847
69    Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys Tyr Ser Arg Gln Phe
70        215              220              225
71    tcc ctg gag cac gtc cac ggc tcg ggc ccc tac tcg gcc ccc tcc cca    895
72    Ser Leu Glu His Val His Gly Ser Gly Pro Tyr Ser Ala Pro Ser Pro
73    230              235              240              245
74    gcc tac agc agc tcc agc ctc tac gcc cct gat gct gtg gcc agc tct    943
75    Ala Tyr Ser Ser Ser Ser Leu Tyr Ala Pro Asp Ala Val Ala Ser Ser
76                    250              255              260
77    gga ccc atc atc tcc gac atc acc gag ctg gct cct gcc agc ccc atg    991
78    Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala Pro Ala Ser Pro Met
79                    265              270              275
80    gcc tcc ccc ggc ggg agc ata gac gag agg ccc cta tcc agc agc ccc    1039
81    Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro Leu Ser Ser Ser Pro
82                    280              285              290
83    ctg gtg cgt gtc aag gag gag ccc ccc agc ccg cct cag agc ccc cgg    1087
84    Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro Pro Gln Ser Pro Arg
85        295              300              305
86    gta gag gag gcg agt ccc ggg cgc cca tct tcc gtg gac acc ctc ttg    1135
87    Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser Val Asp Thr Leu Leu
88    310              315              320              325
89    tcc ccg acc gcc ctc att gac tcc atc ctg cgg gag agt gaa cct gcc    1183
90    Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg Glu Ser Glu Pro Ala
91                    330              335              340
92    ccc gcc tcc gtc aca gcc ctc acg gac gcc agg ggc cac acg gac acc    1231
93    Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg Gly His Thr Asp Thr
94                    345              350              355
95    gag ggc cgg cct ccc tcc ccc ccg ccc acc tcc acc cct gaa aag tgc    1279
96    Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser Thr Pro Glu Lys Cys
97                    360              365              370
```

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```
98      ctc agc gta gcc tgc ctg gac aag aat gag ctc agt gac cac ttg gat      1327
99      Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu Ser Asp His Leu Asp
100          375                 380                 385
101     gct atg gac tcc aac ctg gat aac ctg cag acc atg ctg agc agc cac      1375
102     Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr Met Leu Ser Ser His
103         390                 395                 400                 405
104     ggc ttc agc gtg gac acc agt gcc ctg ctg gac ctg ttc agc ccc tcg      1423
105     Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp Leu Phe Ser Pro Ser
106                 410                 415                 420
107     gtg acc gtg ccc gac atg agc ctg cct gac ctt gac agc agc ctg gcc      1471
108     Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu Asp Ser Ser Leu Ala
109             425                 430                 435
110     agt atc caa gag ctc ctg tct ccc cag gag ccc ccc agg cct ccc gag      1519
111     Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg Pro Pro Glu
112             440                 445                 450
113     gca gag aac agc agc ccg gat tca ggg aag cag ctg gtg cac tac aca      1567
114     Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln Leu Val His Tyr Thr
115         455                 460                 465
116     gcg cag ccg ctg ttc ctg ctg gac ccc ggc tcc gtg gac acc ggg agc      1615
117     Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser Val Asp Thr Gly Ser
118     470                 475                 480                 485
119     aac gac ctg ccg gtg ctg ttt gag ctg gga gag ggc tcc tac ttc tcc      1663
120     Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu Gly Ser Tyr Phe Ser
121                 490                 495                 500
122     gaa ggg gac ggc ttc gcc gag gac ccc acc atc tcc ctg ctg aca ggc      1711
123     Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu Leu Thr Gly
124             505                 510                 515
125     tcg gag cct ccc aaa gcc aag gac ccc act gtc tcc tagaggcccc          1757
126     Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val Ser
127             520                 525
128     ggaggagctg ggccagccgc ccacccccac ccccagtgca gggctggtct tggggaggca   1817
129     gggcagcctc gcggtcttgg gcactggtgg gtcggccgcc atagcccccag taggacaaac   1877
130     gggctcgggt ctgggcagca cctctggtca ggagggtcac cctggcctgc cagtctgcct   1937
131     tcccccaacc ccgtgtcctg tggtttggtt ggggcttcac agccacacct ggactgaccc   1997
132     tgcaggttgt tcatagtcag aattgtattt tggattttta cacaactgtc ccgttccccg   2057
133     ctccacagag atacacagat atatacacac agtggatgga cggacaagac aggcagagat   2117
134     ctataaacag acaggctcta aaaaaaaaaa aaaaaaaa                           2156
```

136 <210> SEQ ID NO: 2
137 <211> LENGTH: 529
138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapien
140 <400> SEQUENCE: 2

```
141     Met Asp Leu Pro Val Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro
142     1               5                   10                  15
143     Ala Phe Leu Thr Lys Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp
144             20                  25                  30
145     Ala Leu Ile Cys Trp Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp
146         35                  40                  45
147     Gln Gly Gln Phe Ala Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn
```

RAW SEQUENCE LISTING   DATE: 04/19/2002
PATENT APPLICATION: US/10/046,420   TIME: 16:05:07

Input Set : N:\Crf3\RULE60\10046420.raw
Output Set: N:\CRF3\04192002\J046420.raw

```
148          50                    55                    60
149     Asn Met Ala Ser Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys
150     65                    70                    75                    80
151     Val Val His Ile Glu Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp
152                       85                    90                    95
153     Thr Glu Phe Gln His Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu
154                      100                   105                   110
155     Glu Asn Ile Lys Arg Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu
156                  115                   120                   125
157     Asp Ile Lys Ile Arg Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val
158                  130                   135                   140
159     Gln Leu Met Lys Gly Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala
160     145                   150                   155                   160
161     Met Lys His Glu Asn Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg
162                       165                   170                   175
163     Gln Lys His Ala Gln Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe
164                      180                   185                   190
165     Leu Ile Ser Leu Val Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys
166                  195                   200                   205
167     Ile Pro Leu Met Leu Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys
168     210                   215                   220
169     Tyr Ser Arg Gln Phe Ser Leu Glu His Val His Gly Ser Gly Pro Tyr
170     225                   230                   235                   240
171     Ser Ala Pro Ser Pro Ala Tyr Ser Ser Ser Ser Leu Tyr Ala Pro Asp
172                      245                   250                   255
173     Ala Val Ala Ser Ser Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala
174                      260                   265                   270
175     Pro Ala Ser Pro Met Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro
176                  275                   280                   285
177     Leu Ser Ser Ser Pro Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro
178         290                   295                   300
179     Pro Gln Ser Pro Arg Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser
180     305                   310                   315                   320
181     Val Asp Thr Leu Leu Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg
182                  325                   330                   335
183     Glu Ser Glu Pro Ala Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg
184                  340                   345                   350
185     Gly His Thr Asp Thr Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser
186                  355                   360                   365
187     Thr Pro Glu Lys Cys Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu
188         370                   375                   380
189     Ser Asp His Leu Asp Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr
190     385                   390                   395                   400
191     Met Leu Ser Ser His Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp
192                      405                   410                   415
193     Leu Phe Ser Pro Ser Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu
194                      420                   425                   430
195     Asp Ser Ser Leu Ala Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro
196                  435                   440                   445
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/046,420

DATE: 04/19/2002
TIME: 16:05:07

Input Set : N:\Crf3\RULE60\10046420.raw
Output Set: N:\CRF3\04192002\J046420.raw

```
197        Pro Arg Pro Pro Glu Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln
198            450                 455                 460
199        Leu Val His Tyr Thr Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser
200        465                 470                 475                 480
201        Val Asp Thr Gly Ser Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu
202                        485                 490                 495
203        Gly Ser Tyr Phe Ser Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile
204                    500                 505                 510
205        Ser Leu Leu Thr Gly Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val
206            515                 520                 525
207        Ser
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 25
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: A heat shock element. A nucleic acid molecule
215       that binds with a heat shock transcription factor
216       to stimulate gene expression
217 <220> FEATURE:
218 <221> NAME/KEY: misc_feature
219 <222> LOCATION: (1)...(25)
220 <223> OTHER INFORMATION: n = A,T,C or G
221 <400> SEQUENCE: 3
```

W--> 222   ngaannttcn nnnnnttcn ngaan   25

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/19/2002
PATENT APPLICATION: US/10/046,420   TIME: 16:05:08

Input Set : N:\Crf3\RULE60\10046420.raw
Output Set: N:\CRF3\04192002\J046420.raw

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,5,6,10,11,12,13,14,15,16,20,21,25

VERIFICATION SUMMARY   DATE: 04/19/2002
PATENT APPLICATION: **US/10/046,420**   TIME: 16:05:08

Input Set : **N:\Crf3\RULE60\10046420.raw**
Output Set: **N:\CRF3\04192002\J046420.raw**

L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0